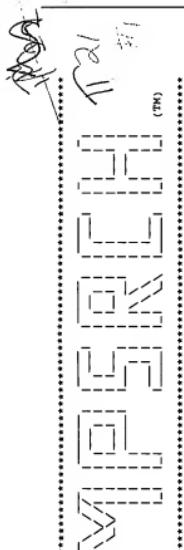


119	GRIOTENKRANSE -SN -O -SPE -NG -GEFLP -GOTTA/PASTYRAKLAASS	Oy
178	LJAKRANSER/LJALSKORS/OLVERBEN/PRASSKOS/LAKPLA/LJOKHÖRS	DB
179	LLVURR -...- A -V -SODA/GEDEBEVRASSKOS/LJOKS/LJALSHÖDHT	Oy
238	TULPANG/CONIGEKA/VANPRASSKOS/EN/POUNTY/TEPNU/PAUT/DE/CORNT	DB
223	SLEVER/GHEYDOKKA -SLEP - -QEVIC/QVHT/TTOFOF/LAT/GOES/LGRANTT	Oy
284	PLATNDYGPMSIT/ILP/DTWYVKEUT/UNGOT/HMECS/URLETFED/DVYAMIC	DB
276	PLATLDO/LJALSHÖST/LP/ADY/VEKTE/US/EKTE/THMEECS/NR/LGT/GREDA/YVNGO	Oy
356	H	DB
338	H	Oy

RESULT #	2	PRELIMINARY:	PPR:	579 Aa.
ID	0121596			
AC	Q121596			
DT	01-NOV-1996	(TREMBLRL. 01, Created sequence)		
DT	01-NOV-1996	(TREMBLRL. 01, Last sequence update)		
DT	01-NOV-1999	(TREMBLRL. 12, Last annotation update)		
DB	GOLDCATMLAE G3 (EC 3.2.1.3).			
OS	Corticinol rolifoli			
OC	Sabatia	Fungi; Basidiomycota; Hymanomycetes; Stereales;		
CC	Corticinolaceae; Corticiaceum.			
BP	INFLUENCE FROM N. A.			
RC	STRAINNAME06271			
RX	96154871			
MEDLINE:				
RA	MURAKAMI, N., KIMURA, A., SUTO, M., YOKOTA, A., TOMITA, F.: Cloning of Corticinol rolifoli cDNA and its expression in Saccharomyces cerevisiae. /			

Bacillus; Firmicutes; Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
[1] IRN IRN
SEQUENCE FROM N.-A.



Release 3.1h. John F. Collins, Biocomputing Research Unit.

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NPBch_PP protein - protein databases search, using Smith-Waterman algorithm

Run on: Wed Apr 12 07:52:24 2000; Mspair time 7.02 Seconds

Tabular output not generated.

Title: 295-09-216-268-17

Description: (1:119), from US69971626B1-pep

Perfect Score: 892

Scoring table: PAM 150

Query: 1 GTSFSVLSVSSDPSLPP.....LGDFSPCVWLRKKEYMR 119

Searched: 188953 seqs, 21686106 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: a-genetics5q

Statistics: Mean 29.971; Variance 126.276; scale 0.237

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	DB	ID	Description	Pred. No.
1	H. pylori	85.5	98	1	W85614		Secreted protein clone 3.13e-63	-----
2	H. pylori	420	471	56	1	W13150	Human secreted protein 1.9e-29	DR
3	H. pylori	210	241	56	1	W13151	Human secreted protein 1.9e-29	DR
4	H. pylori	93	104	48	1	W21409	WABH dehydrogenase subunit 1.22e-01	DR
5	H. pylori	88	99	51	1	W27355	Rabbit interferon gamma 2.13e-01	DR
6	H. pylori	88	99	167	1	W7355	Rabbit interferon gamma 2.91e+01	DR
7	H. pylori	87	98	336	1	W23397	TWAK-1 proteasum chain 3.4e+01	DR
8	H. pylori	86	95	573	1	W32884	Parainfluenza virus type 4.1e+01	CC
9	H. pylori	85	95	573	1	W42667	H. pylori cytoplasmic 4.1e+01	CC
10	H. pylori	85	95	341	1	W02210	H. pylori cytoplasmic 4.1e+01	CC
11	H. pylori	83	93	341	1	W02211	H. pylori cytoplasmic 6.8e+01	CC
12	H. pylori	83	93	463	1	W88335	E. coli G157:H7 F12 re 6.8e+01	CC
13	H. pylori	83	93	520	1	W02621	O antigen fliPase inv 6.8e+01	CC
14	H. pylori	82	92	137	1	W07592	Mouse acetylcholine re 6.8e+01	CC
15	H. pylori	81	92	193	1	W07593	Recombinant Lyphtoxin 8.7e+01	CC
16	H. pylori	81	92	500	1	W07594	H. pylori cell envelop 8.7e+01	CC
17	H. pylori	81	92	522	1	W07595	H. pylori cell envelop 9.5e+01	CC
18	H. pylori	81	92	523	1	W07596	Outer membrane protein 9.5e+01	CC
19	H. pylori	81	92	546	1	W07597	Human purinergic receptor 9.5e+01	CC
20	H. pylori	81	92	476	1	R70099	Lettuce infectious yell 9.5e+01	CC
21	H. pylori	81	92	967	1	W93211	Human CD13/aminopeptidase 9.5e+01	CC
22	H. pylori	80	90	31	1	W97645	Breast-specific BS202 1.13e+02	CC
23	H. pylori	80	90	39	1	W13175	Human secreted protein 1.13e+02	CC

Sequence: 98 AA;

Length: 98;

Score: 763; DB 1; Length: 98;

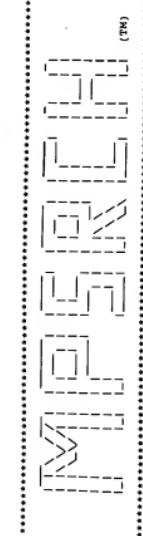
Query Match Similarity: 100.0%; Pred: 0; Mismatches: 0; Indels: 0; Gaps: 0;

Best Local Similarity: 100.0%; Matches: 98; Conservative: 0;

db: 1 MSLACQCPPLAQCTIVSIAWQVIMLIDMIZIFPVNSAVLIEDPYPTPKDFNPNVITY 60

ALIGNMENTS

RESULT	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726	727	728	729	730	731	732	733	734	735	736	737	738	739	740	741	742	743	744	745	746	747	748	749	750	751	752	753	754	755	756	757	758	759	760	761	762	763	764	765	766	767	768	769	770	771	772	773	774	775	776	777	778	779	780	781	782	783	784	785	786	787	788	789	790	791	792	793	794	795	796	797	798	799	800	801	802	803	804	805	806	807	808	809	810	811	812	813	814	815	816	817	818	819	820	821	822	823	824	825	826	827	828	829	830	831	832	833	834	835	836	837	838	839	840	841	842	843	844	845	846	847	848	849	850	851	852	853	854	855	856	857	858	859	860	861	862	863	864	865	866	867	868	869	870	871	872	873	874	875	876	877	878	879	880	881	882	883	884	885	886	887	888	889	890	891	892	893	894	895	896	897	898	899	900	901	902	903	904	905	906	907	908	909	910	911	912	913	914	915	916	917	918	919	920	921	922	923	924	925	926	927	928	929	930	931	932	933	934	935	936	937	938	939	940	941	942	943	944	945	946	947	948	949	950	951	952	953	954	955	956	957	958	959	960	961	962	963	964	965	966	967	968	969	970	971	972	973	974	975	976	977	978	979	980	981	982	983	984	985	986	987	988	989	990	991	992	993	994	995	996	997	998	999	1000



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MPArch_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Apr 12 08:04:32 2000: MaxPar time 13.26 Seconds

Title: 205-00-276-268-20
Tabular output from Smith-Waterman algorithm

Description: (11-17) From US09276268-PP

Sequence: 1 MHSQANTPLARLKVWFGS.....KRAAGAGYKPKNSQAKAQAK 317

Scoring table: Gap 150

Searched: 188933 seqs, 23686106 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: a_genomeSeq

l_genomeSeq

Statistics: Mean 33.327; Variance 130.318; scale 0.256

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query No.	Score	Match Length	DB ID	Description	Predef. No.
1	1535	56.2	263 1	Y01988 Human follistatin-3 pr	6.11e-155
2	319	55.2	112 1	Follistatin.	1.22e-70
3	789	33.2	64 1	Human follistatin (HFS	6.8e-10
4	783	33.0	304 1	Human follistatin Protein	1.8e-69
5	783	32.9	R20063 1	Human follistatin	1.8e-69
6	778	32.7	R20061 1	Pig FGF-binding protein	1.0e-68
7	510	21.4	R07524 1	Human polypeptide chain elongation factor 1A	2.54e-40
8	505	21.3	462 1	W41123 Elongation Factor 1A	6.6e-40
9	496	19.8	305 1	Prostate tumor-induc	7.0e-39
10	429	19.6	M03158 1	yeast elongation facto	3.79e-32
11	393	16.5	293 1	Plant elongation factor 1	3.59e-28
12	392	16.5	R11584 1	61-1 clathrin subunit	3.59e-28
13	392	16.5	458 1	Translational elongation	4.55e-28
14	388	16.3	R05569 1	Plant elongation facto	1.11e-27
15	388	16.3	448 1	Lef2-1 protein.	1.11e-27
16	388	16.3	R11594 1	Lef2-1 clone A polype	4.48e-27
17	388	16.3	664 1	Plastid elongation facto	1.11e-27
18	388	16.3	W41123 1	Protein kinase C epsilon	1.11e-27
19	170	7.1	W17860 1	Follistatin related pr	4.03e-18
20	169	7.1	W09406 1	Transforming growth fa	6.55e-16
21	160	6.7	W17508 1	Human Gsp1-TR.	3.35e-05
22	160	6.7	W01564 1	Sequence of human bone	3.12e-05
23	140	5.9	W07663 1	Human transforming gro	2.21e-03

RESULT

ID Y01988 standard protein; 263 AA.

AC Y01988.

DT 11-JUN-1999 (first entry)

DE Human follistatin-3 protein sequence.

KW follistatin-3; Human; cancer; cellular growth disorder; liver cirrhosis;

KW differentiation disorder; reproductive system disorder; male sterility;

KW activin-induced differentiation inhibitor; gonadotroph adenoma; hepatoma;

KW fibroblast; chondroblast; chondrocyte; pulmonary fibrosis; tumor;

KW sebaceous gland; skin neoplasms; metastasis; infectious disease;

KW fibroblast; osteoblast; osteoarthritis; shock; therapy.

CC Homo sapiens.

OS Homo sapiens.

PN N0931034-A.

PD 04-KAN-1999.

PP 27-JUN-1999; 017710-0009.

PR (1) HUMAN GROWTH SCI INC.

PI Duan R, Ruben SH.

NP/ 99-204464-17.

DR N-PDB; X28124.

DR N-PSD; X28124.

PP products for treating e.g. cancers, male sterility, wound healing,

immunotherapy, disorders, angiogenesis and autoimmune, inflammatory and

infective disorders; and autoimmunity.

Claim 1B: FIG 1: (Oppg; English)

This sequence is the follistatin-3 (PS3) protein of the invention.

The products can be used to treat cancers and other cellular growth and

differentiation disorders as well as disorders of the reproductive

system PS3 can be used or to treat male sterility. PS3 may also be used to

to inhibit the activity-induced differentiation of follicular endothelial

cell activity, it may be therapeutically useful to regulate autocrine endothelial

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Best Local Similarity	79.41	Pred. No.	1.01e+143	2;
Matches	201	Conservative	27	Mismatches 23
		Indels	2	Gaps 2;
6	PEPLAPFLGALAWVGFSS-MSQSRPAGYQVQDQEQATSLVQDFTYRACCS 64			
3	SQAFPLAQLRGLWVTFQVASSSSEPSQVQDQEATCSDVLTYSRBCSCAS 62			
65	GTDQDNHMTKIPKINTLQFGVLLCIPKQDSDVCPKTCAGMGRP-CDCAP 123			
63	GHYIANTMSPKTSITLQFGVLLCIPKQDSDVCPKTCAGMGRP-GASNCVCP 122			
124	DQCSLNLNGSGATDTRBFLBRANCHDPSDTRBFLBRANCHDPSDTRBFLBRANCHDPS 183			
123	NESQPGPAPVQGSDATTDRECLAYTARCGHPPLWVYNGVQGSDATTDRECLAYTARCGHPPLWVYNGVQGSD 182			
184	VQDGSAICWVRACPCPSPSSQDLCNNNTYISCHHQRCATGSRISGHRAGSC 24.3			
183	VQDGSAICWVRACPCPSPSSQDLCNNNTYISCHHQRCATGSRISGHRAGSC 24.2			
244	ACTPPGQESA 256			
243	TGGPKFLSDAA 255			
SPLIT	2	US-08-972-008-5	STANDARD:	PRT: 73 AA.
xxxxxx				
Sequence 5, Application US/08972008				
Sequence 5, Application US/08972008				
Patent No. 5912120				
GENERAL INFORMATION:				
NAME OF INVENTOR(S): Douglas A. No. 5912420 No. Molecules of the Polylisterin-Related				
NUMBER OF SEQUENCES: 5				
CORRESPONDENCE ADDRESS:				
ADDRESSSES: LAHIVE & COCKFIELD, LLP				
STREET: 28 State Street				
STATE: Massachusetts				
COUNTRY: USA				
COMPUTER READABLE FORM:				
MEDIUM: Floppy disk				
OPERATING SYSTEM: PC compatible DOS				
SOFTWARE: Patent In Release 11.0, Version 1.1.25				
CURRENT APPLICATION NUMBER: US/08/972,008				
FILING DATE:				
ISSUE DATE:				
ATTORNEY/AGENT/THON: A.5				
NAME: Alan E. Madrigal				
REGISTRATION NUMBER: 16,207				
REFERENCE/DOCKET NUMBER: NH-026				
TELECOMMUNICATION INFORMATION:				
TELEPHONE: (617) 227-7400				
TELEFAX: (617) 227-7411				
TELETYPE: (617) 227-7400				
TELEMAIL: NH-026@MIT.EDU				
INFORMATION FOR SEQ ID NO: 5:				
SEQUENCE CHARACTERISTICS:				
LENGTH: 73 amino acids				
TYPE: amino acid				
TOPOLOGY: linear				
FRAGMENT: peptide				
SEQUENCE: 73 AA: Y674 NH: 26282 CN: 5				
Match Similarity 90.44%; Score 519; DB 21; Length 73;				
21.88; Score 519; DB 21; Length 73;				
Match Similarity 90.44%; Score 1.41e+38;				